#5

SEQUENCE LISTING

<110> Yamamoto, Hirokazu
Kimoto, Norihiro

<120> NOVEL ENONE REDUCTASES, METHODS FOR PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A CARBON-CARBON DOUBLE BOND OF AN ALPHA,BETA-UNSATURATED KETONE USING THE REDUCTASES

<130> 06501-100001

<140> US 10/081,644
<141> 2002-02-21

<150> JP 2001-49363
<151> 2001-02-23

<160> 29

<170> FastSEQ for Windows Version 4.0

A2

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<212> DNA
<213> Kluyveromyces lactis

<220>
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<222> (1)...(1110)

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gct gtt gtt aaa aca gat gtc tca gtt cca gaa tta aag gag ggt aca       96
Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr
            20                  25                  30

gcc ttg gtg aag gtt gag gct gtt gct ggt aac cca act gat tgg aag      144
Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys
        35                  40                  45

cat att gct tat aag att ggt cca gaa ggt tca att cta gga tgt gac      192
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp
    50                  55                  60

att gct ggt aca gtt gtc aaa ctt gga cca aat gct agt act gac ttg      240
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu
65                  70                  75                  80

aag gtt gga gat acc ggt ttc ggt ttt gtt cac ggt gct tcc caa aca      288
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr
                85                  90                  95
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gat cct aaa aat ggt gca ttt gct gaa tat gcc agg gtt tat cca cct 336
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro
100 105 110

ttg ttt tac aag agt aac tta act cac tca act gct gat gaa att tct 384
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser
115 120 125

gaa ggc cct gtg aag aac ttc gaa tct gct gca tca ttg cca gtt tcg 432
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser
130 135 140

ttg aca act gct ggt gtt agt ttg tgt cat cac ttg ggc tca aaa atg 480
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met
145 150 155 160

gaa tgg cac cca tct acc ccg caa cat act cat cca tta ttg att tgg 528
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp
165 170 175

ggt ggt gct aca gca gtg ggt caa caa cta atc caa gtt gcc aaa cat 576
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His
180 185 190

A2

atc aat gct tat act aag att gta act gtt gct tct aaa aag cat gaa 624
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu
195 200 205

aag ctt tta aag tct tat ggt gct gat gat gtc ttt gac tat cat gat 672
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp
210 215 220

gca ggc gtt att gag cag atc aaa tcg aag tat cca aac ctg caa cat 720
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His
225 230 235 240

gtt att gac gct gtg gga agc gaa gat agt atc ccc gag gcc tat aaa 768
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys
245 250 255

gtc aca gca gat agt cta cct gcc aca tta tta gaa gtg gtt cca atg 816
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met
260 265 270

acc att gaa agc att cct gaa gaa atc aga aaa gat aat gtt aaa att 864
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile
275 280 285

gat att act ttg ttg tat cgt gca tct ggt caa gaa att cta ttg ggt 912
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly
290 295 300

gca aca aga ttt cct gct agt cca gaa tat cat gaa gcc aca gtt aaa 960
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys
305 310 315 320

ttc gtt aag ttt ata aat cca cac ctt aac aac ggt gat atc cat cat 1008

Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His
325 330 335

atg aat att aaa gtt ttc agc aac ggc tta gat gat gtc cca gct ctc 1056
Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp.Asp Val Pro Ala Leu
340 345 350

act gaa ggt ata aaa gaa ggt aaa aac aaa aat gtt aag tat gtt gcc 1104
Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala
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agg tta taa 1113
Arg Leu
370

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<213> Kluyveromyces lactis

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Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys
35 40 45
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp
50 55 60
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu
65 70 75 80
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr
85 90 95
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro
100 105 110
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser
115 120 125
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser
130 135 140
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met
145 150 155 160
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp
165 170 175
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His
180 185 190
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu
195 200 205
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp
210 215 220
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His
225 230 235 240
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys
245 250 255
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met
260 265 270
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile

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                                                                  285
        275                 280
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly
    290                 295                 300
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys
305                 310                 315                 320
Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His
                325                 330                 335
Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu
            340                 345                 350
Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala
        355                 360                 365
Arg Leu
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<211> 1145
<212> DNA
<213> Saccharomyces cerevisiae

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<222> (6)...(1133)

A2

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       1               5                  10                  15

aat ggc aag gct gta gtc aaa cag gac att cca att cct gaa tta gaa      98
Asn Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu
            20                  25                  30

gaa gga ttt gtt cta att aag act gtc gcc gtt gcc ggt aac cct acc     146
Glu Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr
        35                  40                  45

gat tgg aaa cat att gat ttc aag att ggt cct caa ggt gcc ctc tta     194
Asp Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu
    50                  55                  60

ggc tgt gat gca gcc ggc caa atc gta aag ttg ggc cca aat gtt gat     242
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp
65                  70                  75

gct gca cgc ttt gcc att ggt gat tac att tat ggg gtt att cac ggt     290
Ala Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly
            80                  85                  90                  95

gct tca gtg agg ttc ccc tca aac ggt gcc ttt gct gag tac tct gcc     338
Ala Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
                100                 105                 110

att tca tcc gag act gct tat aaa cca gcc aga gag ttt aga ttg tgc     386
Ile Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys
            115                 120                 125

ggt aaa gac aag cta cca gaa ggc ccc gta aaa tct tta gaa ggg gca     434
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Gly Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala
130 135 140

gta tcc ctc cca gtc tca ttg acc acg gct ggt atg atc ctt aca cat 482
Val Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His
145 150 155

agt ttt ggc ttg gac atg aca tgg aag ccc tcc aaa gcg caa aga gat 530
Ser Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp
160 165 170 175

caa ccc atc tta ttt tgg ggt ggt gcc act gct gtt ggc cag atg ctt 578
Gln Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu
180 185 190

att caa ttg gca aaa aaa cta aac ggt ttc agc aag atc atc gtc gtt 626
Ile Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val
195 200 205

gct tct cgt aaa cat gaa aaa ttg ttg aaa gag tac ggt gca gat gaa 674
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
210 215 220

ctt ttt gac tac cac gat gct gac gtt atc gaa cag ata aaa aag aag 722
Leu Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys
225 230 235

A2

tac aac aac att cct tac ttg gtg gac tgt gtc tcc aac aca gaa act 770
Tyr Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr
240 245 250 255

att caa cag gtg tac aaa tgt gcc gct gat gac tta gac gct acg gtc 818
Ile Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val
260 265 270

gtt caa ttg acc gtt tta acc gaa aaa gat atc aag gag gaa gac agg 866
Val Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg
275 280 285

agg caa aac gtc agt att gaa gga acc ctt cta tat ttg ata gga ggt 914
Arg Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly
290 295 300

aac gac gtc cca ttt ggc acg ttt act ttg cca gca gac cct gaa tac 962
Asn Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr
305 310 315

aag gaa gcc gcc ata aaa ttt att aag ttc atc aat cca aaa atc aat 1010
Lys Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
320 325 330 335

gat ggt gaa atc cac cac atc cca gtg aaa gtt tac aag aac ggg tta 1058
Asp Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu
340 345 350

gat gat atc cca cag tta ctt gat gat att aag cac ggg agg aat tct 1106
Asp Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser

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            355                 360                 365

ggc gaa aag ttg gtt gcc gtc ttg aaa taatctagac tg                  1145
Gly Glu Lys Leu Val Ala Val Leu Lys
        370                 375


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<212> PRT
<213> Saccharomyces cerevisiae

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            20                  25                  30
Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr Asp
        35                  40                  45
Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu Gly
    50                  55                  60
Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp Ala
65                  70                  75                  80
Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly Ala
                85                  90                  95
Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile
            100                 105                 110
Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys Gly
        115                 120                 125
Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala Val
    130                 135                 140
Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His Ser
145                 150                 155                 160
Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp Gln
                165                 170                 175
Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu Ile
            180                 185                 190
Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val Ala
        195                 200                 205
Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu Leu
    210                 215                 220
Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys Tyr
225                 230                 235                 240
Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr Ile
                245                 250                 255
Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val Val
            260                 265                 270
Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg Arg
        275                 280                 285
Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly Asn
    290                 295                 300
Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr Lys
305                 310                 315                 320
Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn Asp
                325                 330                 335
Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu Asp
            340                 345                 350
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Glu Lys Leu Val Ala Val Leu Lys
370 375

<210> 5
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<212> DNA
<213> Saccharomyces cerevisiae

<220>
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<222> (1)...(1131)

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gac ggt aaa gcg gtt gtt aaa gag ggc att ccc att cct gaa ttg gaa 96
Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu
20 25 30

A2 gaa gga ttc gta ttg att aag aca ctc gct gtt gct ggt aac ccc act 144
Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr
35 40 45

gat tgg gca cac att gac tac aag atc ggg cct caa gga tct att ctg 192
Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu
50 55 60

gga tgt gat gct gct ggc caa att gtc aaa ttg ggc cca gct gtc aat 240
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn
65 70 75 80

cct aaa gac ttt tct atc ggt gat tat att tat ggg ttc att cac gga 288
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly
85 90 95

tct tcc gta agg ttt cct tcc aat ggt gct ttt gct gaa tat tct gct 336
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
100 105 110

att tca act gtg gtt gcc tac aaa tca ccc aat gaa ctc aaa ttt ttg 384
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu
115 120 125

ggt gag gat gtt cta cct gcc ggc cct gtc agg tct ttg gaa ggt gta 432
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val
130 135 140

gcc act atc cca gtg tca ctg acc aca gcc ggc ttg gtg ttg acc tat 480
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr
145 150 155 160

aac ttg ggc ttg gac ctg aag tgg gag cca tca acc cca caa aga aaa 528
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys

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                165                 170                 175

ggc ccc atc tta tta tgg ggc ggt gca act gca gta ggt cag tcg ctc      576
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu
            180                 185                 190

atc caa tta gcc aat aaa ttg aat ggc ttc acc aag atc att gtt gtg      624
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val
        195                 200                 205

gct tct cgg aag cac gaa aaa ctt ttg aaa gaa tat ggt gct gat gaa      672
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
    210                 215                 220

tta ttt gat tat cat gat att gac gtg gta gaa caa att aaa cac aag      720
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys
225                 230                 235                 240

tac aac aat atc tcg tat tta gtc gac tgt gtc gcg aat caa gat acg      768
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr
                245                 250                 255

ctt caa caa gtg tac aaa tgt gcg gcc gat aaa cag gat gct aca att      816
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile
            260                 265                 270

gtt gaa tta aaa aat ttg aca gaa gaa aac gtc aaa aaa gag aac agg      864
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg
        275                 280                 285

aga caa aac gtt act att gac ata ata agg cta tat tca ata ggt ggc      912
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly
    290                 295                 300

cat gaa gta cca ttt gga aac att act tta cca gcc gac tca gaa gct      960
His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala
305                 310                 315                 320

agg aaa gct gca ata aaa ttt atc aaa ttc atc aat cca aag att aat     1008
Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
                325                 330                 335

gat gga caa att cgc cat att cca gta agg gtc tat aag aac ggg ctt     1056
Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu
            340                 345                 350

tgt gat gtt cct cat atc cta aaa gac atc aaa tat ggt aag aac tct     1104
Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser
        355                 360                 365

ggt gaa aaa ctc gtt gcc gta tta aac taa                            1134
Gly Glu Lys Leu Val Ala Val Leu Asn
    370                 375
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<212> PRT
<213> Saccharomyces cerevisiae

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            20                  25                  30
Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr
        35                  40                  45
Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu
    50                  55                  60
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn
65                  70                  75                  80
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly
                85                  90                  95
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
            100                 105                 110
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu
        115                 120                 125
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val
    130                 135                 140
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr
145                 150                 155                 160
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys
                165                 170                 175
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu
            180                 185                 190
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val
        195                 200                 205
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
    210                 215                 220
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys
225                 230                 235                 240
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr
                245                 250                 255
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile
            260                 265                 270
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg
        275                 280                 285
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly
    290                 295                 300
His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala
305                 310                 315                 320
Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
                325                 330                 335
Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu
            340                 345                 350
Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser
        355                 360                 365
Gly Glu Lys Leu Val Ala Val Leu Asn
    370                 375
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<211> 1122
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (7)...(1110)

<400> 7

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        1               5                  10

gag ggc gtt ccc att cct gaa ttg gaa gaa gga ttc gta ttg att aag          96
Glu Gly Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys
 15                  20                  25                  30

aca ctc gct gtt gct ggt aac ccg act gat tgg gca cac att gac tac         144
Thr Leu Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr
                 35                  40                  45

aag gtc ggg cct caa gga tct att ctg gga tgt gac gct gcc ggc caa         192
Lys Val Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln
             50                  55                  60

att gtc aaa ttg ggc cca gcc gtc gat cct aaa gac ttt tct att ggt         240
Ile Val Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly
         65                  70                  75

gat tat att tat ggg ttc att cac gga tct tcc gta agg ttt cct tcc         288
Asp Tyr Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser
     80                  85                  90

aat ggt gct ttt gct gaa tat tct gct att tca act gtg gtt gcc tac         336
Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr
 95                  100                 105                 110

aaa tca ccc aat gaa ctc aaa ttt ttg ggt gaa gat gtt cta cct gcc         384
Lys Ser Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala
                115                 120                 125

ggc cct gtc agg tct ttg gaa ggg gca gcc act atc cca gtg tca ctg         432
Gly Pro Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu
            130                 135                 140

acc aca gct ggc ttg gtg ttg acc tat aac ttg ggc ttg aac ctg aag         480
Thr Thr Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys
        145                 150                 155

tgg gag cca tca acc cca caa aga aac ggc ccc atc tta tta tgg ggc         528
Trp Glu Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly
    160                 165                 170

ggt gca act gca gta ggt cag tcg ctc atc caa tta gcc aat aaa ttg         576
Gly Ala Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu
175                 180                 185                 190

aat ggc ttc acc aag atc att gtt gtg gct tct cgg aaa cac gaa aaa         624
Asn Gly Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys
                195                 200                 205
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ctg ttg aaa gaa tat ggt gct gat caa cta ttt gat tac cat gat att      672
Leu Leu Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile
            210                 215                 220

gac gtg gta gaa caa att aaa cac aag tac aac aat atc tcg tat tta      720
Asp Val Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu
        225                 230                 235

gtc gac tgt gtc gcg aat caa aat acg ctt caa caa gtg tac aaa tgt      768
Val Asp Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys
    240                 245                 250

gcg gcc gat aaa cag gat gct acc gtt gtc gaa tta act aat ttg aca      816
Ala Ala Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr
255                 260                 265                 270

gaa gaa aac gtc aaa aag gag aat agg agg caa aat gtc act att gac      864
Glu Glu Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp
                275                 280                 285

aga aca aga ctg tat tca ata ggc ggc cat gaa gta cca ttt ggt ggc      912
Arg Thr Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly
            290                 295                 300

att act ttc cct gct gac cca gaa gcc agg aga gct gcc acc gaa ttc      960
Ile Thr Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe
        305                 310                 315

gtc aag ttc atc aat cca aag att agt gat ggg caa att cac cat att     1008
Val Lys Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile
    320                 325                 330

cca gca agg gtc tat aag aac ggg ctt tac gat gtt cct cgt atc ctg     1056
Pro Ala Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu
335                 340                 345                 350

gaa gac att aaa atc ggt aag aac tct ggt gaa aaa ctc gtt gcc gta     1104
Glu Asp Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val
                355                 360                 365

tta aac taatctagaa ac                                              1122
Leu Asn
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A2

<210> 8
<211> 368
<212> PRT
<213> Saccharomyces cerevisiae

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Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys Thr Leu
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Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr Lys Val
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        35                  40                  45
Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln Ile Val
    50                  55                  60
Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly Asp Tyr
65                  70                  75                  80
Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser Asn Gly
                85                  90                  95
Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr Lys Ser
            100                 105                 110
Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala Gly Pro
        115                 120                 125
Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu Thr Thr
    130                 135                 140
Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys Trp Glu
145                 150                 155                 160
Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly Gly Ala
                165                 170                 175
Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu Asn Gly
            180                 185                 190
Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys Leu Leu
        195                 200                 205
Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile Asp Val
    210                 215                 220
Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu Val Asp
225                 230                 235                 240
Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys Ala Ala
                245                 250                 255
Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr Glu Glu
            260                 265                 270
Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp Arg Thr
        275                 280                 285
Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly Ile Thr
    290                 295                 300
Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe Val Lys
305                 310                 315                 320
Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile Pro Ala
                325                 330                 335
Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu Glu Asp
            340                 345                 350
Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val Leu Asn
        355                 360                 365
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<400> 9
Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp
 1   5   10

<210> 10
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<400> 10

Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp Ile
1 5 10

<210> 11
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<221> misc_feature
<222> 12
<223> n = g, a, c or t

<400> 11
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<210> 12
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<221> misc_feature
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<223> n = g, a, c or t

<400> 12
atwgghccwg argghtcnat 20

<210> 13
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tcccaaacag atcctaaaaa tggtgcattt gctgaatatg ccagggttta tccacctttg 180

ttttacaaga gtaacttaac tcactcaact gctgatgaaa tttctgaagg ccctgtgaag 240
aacttcgaat ctgctgcatc attgccagtt tcgttgacaa ctgctggtgt tagtttgtgt 300
catcacttgg gctcaaaaat ggaatggcac ccatctaccc cgcaacatac tcatccatta 360
ttgatttggg gtggtgctac agcagtgggt caacaactaa tccaagttgc caaacatatc 420
aatgcttata ctaagattgt aactgttgct tctaaaaagc atgaaaagct tttaaagtct 480
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A2

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<210> 17
<211> 21
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<400> 17
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<210> 18
<211> 23
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<220>
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<400> 18
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<210> 19
<211> 24
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<400> 19
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A2 concludes

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<210> 27
<211> 37
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<210> 29
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